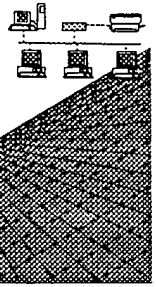


Haimud

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/037,657

Art Unit / Team No. :

1646

Date Processed by STIC:

6/30/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/037,657DATE: 06/30/1999
TIME: 14:43:20

Input Set: I037657.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

*see
p. 5, too*

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Hilton, Douglas J.
2 Nicola, Nicos A.
3 Farley, Alison
4 Wilson, Tracy
5 Zhang, Jian-Guo
6 Alexander, Warren
7 Rakar, Steven
8 Fabri, Louis
9 Kojima, Tetsuo
10 Maeda, Masatsugu
11 Kikuchi, Yasufumi
12 Nash, Andrew
13 <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
14 ENCODING SAME
15 <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
16 <140> CURRENT APPLICATION NUMBER: US/09/037,657
17 <141> CURRENT FILING DATE: 1998-03-10
18 <150> EARLIER APPLICATION NUMBER: 08/928,720
19 <151> EARLIER FILING DATE: 1997-09-11
20 <160> NUMBER OF SEQ ID NOS: 54
21 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO 1
23 <211> LENGTH: 5
24 <212> TYPE: PRT
25 <213> ORGANISM: Unknown
26 <220> FEATURE:
27 <221> NAME/KEY: UNSURE
28 <222> LOCATION: (3)
29 <223> OTHER INFORMATION: Unsure at position 3
30 <400> SEQUENCE: 1
31 Trp Ser Xaa Trp Ser
32 1 5
33 <210> SEQ ID NO 2
34 <211> LENGTH: 24
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Artificial Sequence: M116 probe
39 <400> SEQUENCE: 2
40 actcgtcca gattcccgcc tttt
41 <210> SEQ ID NO 3
42 <211> LENGTH: 24
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence

W-->OK

see item 12 on Err Summary Sheet

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45 <220> FEATURE:
46 <223> OTHER INFORMATION: Description of Artificial Sequence:M108 probe
47 <400> SEQUENCE: 3
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50 <211> LENGTH: 24
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence:M159 probe
55 <400> SEQUENCE: 4
56      ggtacttggc ttggaagagg aaat                24
57 <210> SEQ ID NO 5
58 <211> LENGTH: 24
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial Sequence:M242 probe
63 <400> SEQUENCE: 5
64      cggctcacgt gcacgtcggg tggg                24
65 <210> SEQ ID NO 6
66 <211> LENGTH: 22
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Description of Artificial Sequence:M112 probe
71 <400> SEQUENCE: 6
72      agctgctggt aaagggcttc tc                22
73 <210> SEQ ID NO 7
74 <211> LENGTH: 15
75 <212> TYPE: DNA
76 <213> ORGANISM: Unknown
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
79 <220> FEATURE:
80 <221> NAME/KEY: unsure
81 <222> LOCATION: (1)
82 <223> OTHER INFORMATION: Unsure at position 1
83 <220> FEATURE:
84 <221> NAME/KEY: unsure
85 <222> LOCATION: (7)
86 <223> OTHER INFORMATION: Unsure at position 7
87 <220> FEATURE:
88 <221> NAME/KEY: unsure
89 <222> LOCATION: (10)
90 <223> OTHER INFORMATION: Unsure at position 10
91 <400> SEQUENCE: 7
92      rtccartcr ctcca                15
93 <210> SEQ ID NO 8
94 <211> LENGTH: 15

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RAW SEQUENCE LISTING
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95 <212> TYPE: DNA
96 <213> ORGANISM: Unknown
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
99 <220> FEATURE:
100 <221> NAME/KEY: unsure
101 <222> LOCATION: (1)
102 <223> OTHER INFORMATION: Unsure at position 1
103 <220> FEATURE:
104 <221> NAME/KEY: unsure
105 <222> LOCATION: (7)
106 <223> OTHER INFORMATION: Unsure at position 7
107 <220> FEATURE:
108 <221> NAME/KEY: unsure
109 <222> LOCATION: (10)
110 <223> OTHER INFORMATION: Unsure at position 10
111 <400> SEQUENCE: 8
112      rctccaytcr ctcca                                15
113 <210> SEQ ID NO 9
114 <211> LENGTH: 21
115 <212> TYPE: DNA
116 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence:1944 probe
119 <400> SEQUENCE: 9
120      aagtgtgacc atcatgtgga c                                21
121 <210> SEQ ID NO 10
122 <211> LENGTH: 18
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:2106 probe
127 <400> SEQUENCE: 10
128      ggaggtgtta aggaggcg                                18
129 <210> SEQ ID NO 11
130 <211> LENGTH: 18
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:2120 probe
135 <400> SEQUENCE: 11
136      atgcccgcgg gtcgcccg                                18
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138 <211> LENGTH: 1629
139 <212> TYPE: DNA
140 <213> ORGANISM: Unknown
141 <220> FEATURE:
142 <221> NAME/KEY: CDS
143 <222> LOCATION: (124) .. (1362)
144 <220> FEATURE:

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/037,657

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145 <223> OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1
146 <400> SEQUENCE: 12
147   ggcacgagct tcgctgtccg cgcccagtgga cgcgcgtgcg gacccgagcc ccaatctgca 60
148   ccccgagac tcgccccgc cccataccgg cgttgagtc accgcccgtt gcgcgccacc 120
149   ccc atg ccc gcg ggt cgc ccg gcc ccc gtc gcc caa tcc gcg cgg cgg 168
150       Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
151       1           5           10           15
152   ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216
153   Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
154       20           25           30
155   ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 264
156   Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
157       35           40           45
158   ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312
159   Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
160       50           55           60
161   tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
162   Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
163       65           70           75
164   acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 408
165   Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
166       80           85           90           95
167   acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
168   Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
169       100          105          110
170   cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
171   Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
172       115          120          125
173   gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
174   Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
175       130          135          140
176   atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca 600
177   Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
178       145          150          155
179   ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag 648
180   Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
181       160          165          170          175
182   tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac 696
183   Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
184       180          185          190
185   act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc 744
186   Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
187       195          200          205
188   act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca 792
189   Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
190       210          215          220
191   aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac 840
192   Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
193       225          230          235
194   ccc cca ccc gac gtg cac gtg agc cgc gtt ggg gcc ctg gag gac cag 888

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195      Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
196      240                      245                      250                      255
197      ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc      936
198      Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
199                      260                      265                      270
200      caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg      984
201      Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
202                      275                      280                      285
203      aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc      1032
204      Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
205                      290                      295                      300
206      ctg aag ccc gcc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc      1080
207      Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
208                      305                      310                      315
209      ggg atc tat ggg tgc aaa aag gcg gga atc tgg agc gag tgg agc cac      1128
210      Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
211      320                      325                      330                      335
212      ccc acc gct gcc tcc acc cct cga agt gag cgc ccg gcc ccg gcc gcc      1176
213      Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
214                      340                      345                      350
215      ggg gtg tgc gag ccg ccg gcc gcc gag ccc agc tgc gcc ccg gtg ccg      1224
216      Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
217                      355                      360                      365
218      cgc gag ctc aag cag ttc ctc gcc tgg ctc aag aag cac gca tac tgc      1272
219      Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
220                      370                      375                      380
221      tgc aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag      1320
222      Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
223                      385                      390                      395
224      aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc      1362
225      Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
226      400                      405                      410
227      taaggatagg ccattctcct gctgggtcag acctggaggc tcacctgaat tggagcccct 1422
228      ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa 1482
229      ccacagctttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggtttg 1542
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231      aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1629
232      <210> SEQ ID NO 13
233      <211> LENGTH: 413
234      <212> TYPE: PRT
235      <213> ORGANISM: Unknown
236      <220> FEATURE:
237      <223> OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1
238      <400> SEQUENCE: 13
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240      1                      5                      10                      15
241      Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
242                      20                      25                      30
243      Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
244                      35                      40                      45

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I037657.RAW

| Line | ? Error/Warning | Original Text |
|------|---------------------------------------|---|
| 31 | W "N" or "Xaa" used: Feature required | Trp Ser Xaa Trp Ser |
| 1030 | W "N" or "Xaa" used: Feature required | Leu Arg Leu Val Arg Ser Glu Xaa His Met X |
| 1034 | W "N" or "Xaa" used: Feature required | Leu Xaa Asp Leu Gly Gly Ser His Gln Ser P |
| 1036 | W "N" or "Xaa" used: Feature required | Xaa Cys Pro His Thr Gly Cys Pro Gly Arg |

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/037,657

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: -
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.